

08/06/47

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using SW model

Run on: April 23, 2003, 07:28:09 / Search time 50 Seconds
 (without alignments)
 1543.919 Million cell updates/sec

Title: US-10-034-849-2

Perfect score: 4168
 Sequence: 1 MTEVVFVLDSSYEYVGRKPE...LKASATGQKTLFDLAKSK 803

Scoring table: BLOSUM62
 Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database: 1: p11:*
 2: p12:*
 3: p13:*
 4: p14:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3033.5	72.4	803	2 B56277	DNA-directed DNA p
2	2434	58.1	784	2 E72515	probable DNA-direc
3	2266	53.6	781	2 JC7382	DNA-directed DNA p
4	1581	37.8	781	2 A69312	DNA polymerase BI
5	1287	30.7	764	2 S75407	probable DNA-direc
6	1236.5	29.5	775	2 S35543	DNA-directed DNA p
7	1207.5	28.8	771	2 C75023	DNA polymerase I p
8	1197.5	28.6	775	2 S67920	DNA-directed DNA p
9	965.5	23.1	1312	2 S68593	DNA-directed DNA p
10	955.5	22.8	1235	2 C71210	probable DNA-direc
11	915	21.8	586	2 C69028	DNA-dependent DNA
12	771.5	18.4	1086	2 T40242	DNA-directed DNA p
13	768.5	18.4	1670	2 S71551	DNA-directed DNA p
14	763.5	18.2	1086	2 T43266	DNA-directed DNA p
15	760.5	18.2	1107	1 A41618	DNA-directed DNA p
16	757.5	18.1	1106	1 A39299	DNA-directed DNA p
17	751	17.9	1038	1 JC5757	DNA-directed DNA p
18	749	17.9	1038	1 T18222	DNA polymerase del
19	743.5	17.8	1105	1 S40243	DNA-directed DNA p
20	741.5	17.7	1088	2 T05731	DNA-directed DNA p
21	731.5	17.5	1084	1 S19661	DNA-directed DNA p
22	718.5	17.2	901	2 B84210	DNA polymerase BI
23	713	17.0	1702	2 S42459	DNA-directed DNA p
24	705	16.8	1094	2 S22573	DNA-directed DNA p
25	691.5	16.5	1097	1 RNBYL3	DNA-directed DNA p
26	671	16.0	1634	2 B64410	DNA-directed DNA p
27	649.5	15.5	879	2 A56277	DNA-directed DNA p
28	647.5	15.5	872	2 JC7380	DNA-directed DNA p
29	628.5	15.0	875	2 JC5186	DNA-directed DNA p

30	625.5	14.9	959	2 F72763	probable DNA-direc
31	598.5	14.3	882	2 S23019	DNA-directed DNA p
32	598	14.3	1081	2 T20658	hypothetical prote
33	594.5	14.2	882	2 F90201	DNA polymerase I
34	579.5	13.8	1462	1 DJH0AC	DNA-directed DNA p
35	578	13.8	1465	2 S45628	DNA-directed DNA p
36	569	13.6	787	2 E82237	DNA polymerase II
37	564.5	13.5	844	2 T31321	DNA-directed DNA p
38	527.5	12.6	787	2 G83410	DNA polymerase II
39	526	12.6	3122	2 T17202	DNA-directed DNA p
40	524.5	12.5	1015	1 DJBE2L	DNA-directed DNA p
41	523.5	12.5	1339	1 S20052	DNA-directed DNA p
42	517	12.3	1505	2 S28079	DNA-directed DNA p
43	515	12.3	1009	1 DJBEM2	DNA-directed DNA p
44	511	12.2	1026	2 T03108	DNA-directed DNA p
45	508.5	12.1	1513	2 T28158	probable DNA-direc

ALIGNMENTS

RESULT 1

DNA-directed DNA polymerase (EC 2.7.7.7) II - Pyrodicticum occultum
 C/Species: Pyrodicticum occultum
 C/Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 20-Jun-2000
 C/Accession: B56277
 R/Uemori, T.; Ishino, Y.; Doi, H.; Kato, I.
 J. Bacteriol. 177, 2164-2177, 1995
 A/Title: The hyperthermophilic archaeon Pyrodicticum occultum has two alpha-like DNA po
 A/Reference number: A56277; MUID:95238290; PMID:7721707
 A/Accession: B56277
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-803 <UEM>
 A/Cross-references: GB:D38574; NID:9807829; PIDN:BA07580.1; PID:9807830
 C/Superfamily: herpesvirus DNA-directed DNA polymerase
 C/Keywords: nucleotidyltransferase

Query Match	72.4%; Score 3033.5; DB 2; Length 803;
Best Local Similarity	70.9%; Pred. No. 1.4e-176;
Matches	571; Conservative 106; Mismatches 121; Indels 7; Gaps 5;
QY	1 MTEVVFVLDSSYEYVGRKPEVITWIAENGSRVYLDISFRPFFYALAPGAD--KO 57
DB	1 MTEVVFVLDSSYEYVGRKPEVITWIAENGSRVYLDISFRPFFYALAPGAD--KO 57
QY	58 VACRIALSRPSPITIGVDDGRKYFGRRRLRIKTVLEAVREYRELYKNVDGVEDVL 117
DB	61 IASIRRLSVVSPITIDAKPLDKRFYGRPRKAVKTTMTPEVRRHRYREAVKKBGVDSL 120
QY	118 EADIRPAMVYLDHDLFPPTWYRVEAEPLNKGQFVVDKVVYVKSRRPDLGALAPTKL 177
DB	121 EADIRPAMVYLDHDLFPPTWYRVEAEPLNKGQFVVDKVVYVKSRRPDLGALAPTKL 178
QY	178 PDLRIAPDIEVYSKQSGSPRPDPVIAVXTDQDEVLFIAEGKDDKPIREFVEYVK 237
DB	179 PDLRIAPDIEVYSKQSGSPRPDPVIAVXTDQDEVLFIAEGKDDKPIREFVEYVK 238
QY	238 RDPDITVGNHNPWVPLLRARLIGKLVTRVGAEPSTSVGHVSGRLAVDLY 297
DB	239 RDPDITVGNHNPWVPLLRARLIGKLVTRVGAEPSTSVGHVSGRLAVDLY 298
QY	298 DVAEEMPEIKISLEVAEYLVGMKSKSEVITNMMEIPYMPDPKKRPILLQYARDVVA 357
DB	299 DVAEEMPEIKISLEVAEYLVGMKSKSEVITNMMEIPYMPDPKKRPILLQYARDVVA 358
QY	358 TYGLAEKILPFAIQLSYVTGLPLDQVAMSVGRLEWYLIRAPFKKELVPRVERPEET 417
DB	359 TYGLAEKILPFAIQLSYVTGLPLDQVAMSVGRLEWYLIRAPFKKELVPRVERPEET 418
QY	418 YKGLATLEPLRGVHEVIAVLDFSSMTYPMIMIKYNGPDLVLPFGKCGSC-CGWEPEYK 476

Db 419 YKGAIVLKLKGVHENVVLDFSSMTYPSIMIKYVGPDIIVDDPSECRKYGCCVVAPEVG 478
Qy 477 HRPFRCPGFEKTVLERLELLEKRVRAEMKKCPDPSPEYRLDEKQALKYLANASYGM 536
Db 479 HRPFRSPGFEKTVLERLELLEKRVRAEMKKCPDPSPEYRLDEKQALKYLANASYGM 538
Qy 537 GWSGARMTGRECAAVTAMGSHLIRTAINTAKLKYIGDTSLSFYDPEKVENFIK 596
Db 539 GWSHARMTGRECAAVTAMGSHLIRTAINTAKLKYIGDTSLSFYDPEKVENFIK 598
Qy 597 IIRKELGEITLKKYKRLFTTEBAKRYAGLLEDRIDIVGEAVRGWMCCLAKVQKV 656
Db 599 FVEKELGEITLKKYKRLFTTEBAKRYAGLLEDRIDIVGEAVRGWMCCLAKVQKV 658
Qy 657 VEIYLTSEVNAKAVYKIVKLEEGKVPLEKTYIMKTLSSRLBEYTBAPHVAARM 716
Db 659 AEIYLTGNVDAKISYIRBEVTKOLREGKVPITKLIIMKTLSSRLBEYTBAPHVAARM 718
Qy 717 LSAGRVSPGDKIGYIVYKGGRISSQAMPYFMVQPSQIDVTYVYDHOIIPALIRILGY 776
Db 719 KEAGREVSPGDKIGYIVYKGGRISSQAMPYFMVQPSQIDVTYVYDHOIIPALIRILGY 778
Qy 777 FGITEKKLKASATGQKTLFDFLAKK 801
Db 778 FGITEKKLKASATGQKTLFDFLAKK 802

RESULT 2

B72515
probable DNA-directed DNA polymerase APE2098 - Aeropyrum pernix (strain KI)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C:Accession: B72515
R:Kawarayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Hakiwa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum A:Reference number: A72450; MUID:99310339; PMID:10382966
A:Accession: B72515
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-784 <KAW>
A:Cross-references: DDBJ:AP000063; NID:G5105654; PIDN:BA01109.1; PID:G5105797
A:Experimental source: strain KI
C:Genetics:
A:Gene: APE2098
C:Superfamily: herpesvirus DNA-directed DNA polymerase

Query Match 58.1%; Score 2434; DB 2; Length 784;
Best local similarity 59.1%; Pred. No. 3.7e-140;
Matches 469; Conservative 113; Mismatches 189; Indels 22; Gaps 5;

Qy 17 GKEPVIIWGIAENGERVVLIDRSFRPYFYALLAGADPKQVAKIRALSRSKPSITIGVE 76
Db 3 GSTPVIILMGAGDSRVVVFYGEFRPYFYVLDGSGVGLDQLAAMIRLSRSPSILIVE 62
Qy 77 DDKRYFRRPRVLRITVLPAAVREYRELTVKQVGVDEVLEADIRFAMRYLIDHDLPPP 136
Db 63 RVRRRFIRGRVBAKVTTLVPAVSVREAVRRLGQVADVLEADIRFALRPIIDNLTVM 122
Qy 137 TWYRVAEPLKNGKGFVVKYLV-----KSRPPLVGEALAPTKLPDLRIALFDI 187
Db 123 RMYVAEVEVAVPHGYSVDRAYTISGDIRBDETRIQEDPLKQ-----LRVMARDI 172
Qy 188 EYVSKQSGPRPERDPVIVIAVKTDDGDEVFLIAGKDRKPIREVEYVVKYDPDIITGY 247
Db 173 EYVSKMRPDPKQDVIMIGIQAGGKEIIEAEDRSKCVIAGVREYKSIDPPVITGY 232
Qy 248 NNNHFDMPYLLRRARILGIDVTRVGAPEPTTSVHGVSVYGRANVLVYAAEMPEIK 307
Db 291 NNNHFDMPYLLRRARILGIDVTRVGAPEPTTSVHGVSVYGRANVLVYAAEMPEIK 291
A:EYVSKQSGPRPERDPVIVIAVKTDDGDEVFLIAGKDRKPIREVEYVVKYDPDIITGY 367

Db 292 VKTLEEVADYLGAVKIGERTLTLEMOIGEWYDDPSKREILRKLRDVRSTWGLAEKFLP 351
Qy 368 FALQSLVYVGLPLDYGAMSVGRLEMYVLIIRAFKOKELVNVNVERPEEYRGAVILEPL 427
Db 352 FGABLSGVSLPDDQWAAVGRLEMLIRBAKAGELVNVNVERPEEYRGAVILIRPK 411
Qy 428 RGVHENIAVDFSSMYPNIMIKYVGPDTLVPRGKCGECGCEWABEVKRRFRCPGPF 487
Db 412 PGVHEDIAVDFASMTYPNIMIKYVGPDTLVPRGEEYGESEVYTADEVGHKFRKSPGPF 471
Qy 488 KTVLERLELRKVRAMKKYPPDPSPYRLDERQALKYLANASYGMGSGARMTYCRE 547
Db 472 KTLERFLSWROIRSEMKGPDPSPBYKLLDERQALKYLANASYGMGMPHARMTYCRE 531
Qy 548 CAKAVTAMGSHLIRTAINTAKLKYIGDTSLSFYDPEKVENFIKIRKELGEIK 607
Db 532 CAEVNTAMGSHLIRTAINTAKLKYIGDTSLSFYDPEKVENFIKIRKELGEIK 591
Qy 608 LERVKRLFTTEBAKRYAGLLEDRIDIVGEAVRGWMCCLAKVQKVVEIYLTSEVN 667
Db 592 VDKYRRVFTTEBAKRYAGLLEDRIDIVGEAVRGWMCCLAKVQKVVEIYLTSEVN 651
Qy 668 KAVRYAKIVKLEEGKVPLEKTYIMKTLSSRLBEYTBAPHVAARMKLSAGRVSPGD 727
Db 652 EAVDYANIIIEKLRQGVDMRKLVIMKTLTRPSMTYEAQPHVATALLMERAGIKVEPGA 711
Qy 728 KIGYIVYKGGRISSQAMPYFMVQPSQIDVTYVYDHOIIPALIRILGYFGITEKKLKAS 787
Db 712 KIGYIVYKGGRISSQAMPYFMVQPSQIDVTYVYDHOIIPALIRILGYFGITEKKLKAS 770
Qy 788 ATGQKTLFDFLAKK 800
Db* 771 GR-QSTLDDPMRR 782

RESULT 3

JC7382
DNA-directed DNA polymerase (BC 2.7.7.7) B3 - Sulfitisphaera ohwakensis
N:Alternate names: DNA polymerase alpha, beta, gamma; DNA polymerase I, II, III
C:Species: Sulfitisphaera ohwakensis
C:Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 31-Dec-2000
C:Accession: JC7382
R:Iwai, T.; Kurogawa, N.; Itoh, Y.H.; Kimura, N.; Horiuchi, T.
DNA Res. 7, 243-251, 2000
A:Title: Sequence analysis of three family B DNA polymerases from the thermocacidophil A:Reference number: JC7380
A:Accession: JC7382
A:Molecule type: DNA
A:Residues: 1-781 <IWA>
A:Cross-references: DDBJ:AB032376
C:Comment: This enzyme has both 3'-5' exonuclease and polymerase activities, and play C:Genetics:
A:Gene: B3
C:Keywords: DNA replication; exonuclease; metal binding; nucleotidyltransferase

Query Match 53.6%; Score 2246; DB 2; Length 781;
Best local similarity 54.3%; Pred. No. 9.9e-129;
Matches 432; Conservative 141; Mismatches 203; Indels 20; Gaps 10;

Qy 6 FTVLDSYEVGKEPOVITWGIAENGERVVLIDRSFRPYFYALLAGADPKQVAKIRALS 65
Db 5 FTLLDFSYDVVENKPYIYIWIIDEGNRVVLLEKKFRPYFYALLVDSYNDIRKEITKL 64
Qy 66 SRKSPITGVEDDKKYPGPRVLRITVLPAAVREYRELTVKQVGVDEVLEADIRFAM 125
Db 65 SKRSPITGVEDDKKYPGPRVLRITVLPAAVREYRELTVKQVGVDEVLEADIRFAM 124
Qy 126 RYVLDHDLPTTVRYVAEABLENKMGFRVDKYLVSRRPEPLVGEALAPTKLPDLRIALF 185
Db 125 RYVLDHDLPTTVRYVAEABLENKMGFRVDKYLVSRRPEPLVGEALAPTKLPDLRIALF 177
Qy 186 DIEVSKQSGPRPERDPVIVIAVKTDDGDEVFLIAGKDRKPIREVEYVVKYDPDIIV 245

QY 421 ATVLEPLRGVHENVIAVLDPSMYENIMIKYNGPDTLVPRGKCGCGGMBAPVYKRR 480
 DB 421 ATVLEPLRGVHENVIAVLDPSMYENIMIKYNGPDTLVPRGKCGCGGMBAPVYKRR 480
 QY 481 RCPGPFKTVLELRLRLKRVRAEMKKYPPDSPERYLLDEROKALVYLANASYGMGSG 540
 DB 481 RCPGPFKTVLELRLRLKRVRAEMKKYPPDSPERYLLDEROKALVYLANASYGMGSG 540
 QY 541 ARMYCECAKAVTAMGRHLIRTAINTARKIGLVYIGDTSLEFVYDPEKVENFIKKE 600
 DB 541 ARMYCECAKAVTAMGRHLIRTAINTARKIGLVYIGDTSLEFVYDPEKVENFIKKE 600
 QY 601 ELGFEFKLEKTVNRLFFTEAKKRYAGLLEDRIDIVGEAVRGDMCELAKEVQTKVVEI 660
 DB 601 ELGFEFKLEKTVNRLFFTEAKKRYAGLLEDRIDIVGEAVRGDMCELAKEVQTKVVEI 660
 QY 661 LKTSVNVKAVEYRKIVKLEBEGKVPLEKLVIMKLSKRLSEYTTTEAPHVAAKRLMSAG 720
 DB 661 LKTSVNVKAVEYRKIVKLEBEGKVPLEKLVIMKLSKRLSEYTTTEAPHVAAKRLMSAG 720
 QY 721 YRVSPEGDKIGYIVKGGGRISORAMPYFVYKDPQIDVTYVYDHOIIPALRLIGYFGIT 780
 DB 721 YRVSPEGDKIGYIVKGGGRISORAMPYFVYKDPQIDVTYVYDHOIIPALRLIGYFGIT 780
 QY 781 EKKLKASATGOKTLPDLPLAKSK 803
 DB 781 EKKLKASATGOKTLPDLPLAKSK 803

RESULT 2

US-08-062-368-4
 Sequence 4, Application US/08062368
 Patent No. 5491086

GENERAL INFORMATION:

APPLICANT: Gelfand, David H.
 TITLE OF INVENTION: Purified Thermostable Nucleic Acid
 TITLE OF INVENTION: Polymerases Enzyme From Pyrodicticum Species
 NUMBER OF SEQUENCES: 35
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Hoffmann-La Roche Inc.
 STREET: 340 Kingstland Street
 CITY: Nutley
 STATE: New Jersey
 COUNTRY: U.S.A.
 ZIP: 07110
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/062,368
 FILING DATE: 19930514
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Sias Ph.D., Stacey R.
 REGISTRATION NUMBER: 32,630
 REFERENCE/DOCKET NUMBER: 8584
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (510) 814-2863
 TELEFAX: (510) 814-2977
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 803 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULAR TYPE: DNA (genomic)
 062-368-4

72.3%, Score 3028.5, DB 1, Length 803;

Best Local Similarity 70.8%; Pred. No. 1e-270;
 Matches 570; Conservative 106; Mismatches 122; Indels 7; Gaps 5;

QY 1 MTEVV-FTVLDSYEVVYKPEQVYIINGIAENGRVYLLDSFRYFALLAPGADP--KQ 57-
 DB 1 MTEVTFEVLDSYEVVYKPEQVYIINGIAENGRVYLLDSFRYFALLAPGADP--KQ 57-
 QY 58 VAQRIPLSRKSPYIIGVEDKRYKGPAPRVLAIRTVLPAAVEYELVKNVGVEDVL 117
 DB 61 IAASTRRLSVKSPYIIDKPLDKRYFGAPRAVAKITMIPESVHRVRAVAKIKGVESL 120
 QY 118 EADIFPARRYLIDHLPFTYTVRAEAPLENKGPVNDKVLVYNSRPEYLGALAPTKL 177
 DB 121 EADIFPARRYLIDKRLYFTYTVRAEAPLENKGPVNDKVLVYNSRPEYLGALAPTKL 178
 QY 178 PDLRLIADIEVYSKQSPRPERDPIVIAVKTDDGDEVLFIARCKDRKDIREFVEYK 237
 DB 179 PDLRLIADIEVYSKQSPRPERDPIVIAVKTDDGDEVLFIARCKDRKDIREFVEYK 238
 QY 238 RDPDPIIVGNNHFDWYLLRLRARIIGIKLDYTRRVAAEFTTSYKGVSVPGRLANDLY 297
 DB 239 AADPDPIIVGNNHFDWYLLRLRARIIGIKLDYTRRVAAEFTTSYKGVSVPGRLANDLY 298
 QY 298 DYAEEMPEIKIKSLSEVVAEYLVGMKSSERVIIINWEIPDYMDPKKRPILLQYADDPVA 357
 DB 299 DYAEEMPEIKIKSLSEVVAEYLVGMKSSERVIIINWEIPDYMDPKKRPILLQYADDPVA 358
 QY 358 TYGLAEKILPFAIQLSYVYGLPLDQVGMASVGFLEWYLLRAAFKMKELVPPNVRPEET 417
 DB 359 TYGLAEKILPFAIQLSYVYGLPLDQVGMASVGFLEWYLLRAAFKMKELVPPNVRPEET 418
 QY 418 YRGALVLEPLRGVHENVIAVLDPSMYENIMIKYNGPDTLVPRGKCGCGGMBAPVYKRR 476
 DB 419 YRGALVLEPLRGVHENVIAVLDPSMYENIMIKYNGPDTLVPRGKCGCGGMBAPVYKRR 478
 QY 477 HFRRCPPGPFKTVLELRLRLKRVRAEMKKYPPDSPERYLLDEROKALVYLANASYGM 536
 DB 478 HFRRCPPGPFKTVLELRLRLKRVRAEMKKYPPDSPERYLLDEROKALVYLANASYGM 538
 QY 537 GWSGARWYCRECAKAVTAMGRHLIRTAINTARKIGLVYIGDTSLEFVYDPEKVENFIK 596
 DB 538 GWSGARWYCRECAKAVTAMGRHLIRTAINTARKIGLVYIGDTSLEFVYDPEKVENFIK 598
 QY 597 IIKBELGPEIKLEKYKRLFTEAKKRYAGLLEDRIDIVGEAVRGDMCELAKEVQTKV 656
 DB 598 IIKBELGPEIKLEKYKRLFTEAKKRYAGLLEDRIDIVGEAVRGDMCELAKEVQTKV 658
 QY 657 VEIVLKTSEVNVKAVEYRKIVKLEBEGKVPLEKLVIMKLSKRLSEYTTTEAPHVAAKRL 716
 DB 658 VEIVLKTSEVNVKAVEYRKIVKLEBEGKVPLEKLVIMKLSKRLSEYTTTEAPHVAAKRL 718
 QY 717 LSAGRVSPGDKIGYIVKGGGRISORAMPYFVYKDPQIDVTYVYDHOIIPALRLIGY 776
 DB 718 LSAGRVSPGDKIGYIVKGGGRISORAMPYFVYKDPQIDVTYVYDHOIIPALRLIGY 778
 QY 777 FGIITEKKLKASATGOKTLPDLPLAKSK 801
 DB 778 FGIITEKKLKASATGOKTLPDLPLAKSK 802

RESULT 3

US-08-062-368-2
 Sequence 2, Application US/08062368
 Patent No. 5491086

GENERAL INFORMATION:

APPLICANT: Gelfand, David H.
 TITLE OF INVENTION: Purified Thermostable Nucleic Acid
 TITLE OF INVENTION: Polymerases Enzyme From Pyrodicticum Species
 NUMBER OF SEQUENCES: 35
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Hoffmann-La Roche Inc.
 STREET: 340 Kingstland Street